

WHAT IS CLAIMED IS:

1 1. In a computer system, a method of identifying
2 an unknown base in a sample nucleic acid sequence, said method
3 comprising the steps of:
4 inputting a plurality of probe intensities, each of
5 said probe intensities being associated with a nucleic acid
6 probe;
7 said computer system comparing said plurality of
8 probe intensities wherein each of said plurality of probe
9 intensities is substantially proportional to said associated
10 nucleic acid probe hybridizing with at least one nucleic acid
11 sequence, said at least one nucleic acid sequence including
12 said sample sequence; and
13 calling said unknown base according to results of
14 said comparing step.

1 2. In a computer system, a method of identifying
2 an unknown base in a sample nucleic acid sequence, said method
3 comprising the steps of:
4 inputting a plurality of probe intensities, each of
5 said probe intensities being associated with a nucleic acid
6 probe;
7 said computer system comparing said plurality of
8 probe intensities wherein each of said plurality of probe
9 intensities is substantially proportional to said associated
10 nucleic acid probe hybridizing with said sample sequence; and
11 calling said unknown base according to results of
12 said comparing step.

1 3. The method of claim 2, wherein said comparing
2 step includes the step of said computer system calculating a
3 ratio of a higher probe intensity to a lower probe intensity.

1 4. The method of claim 3, wherein said calling
2 step includes the step of calling said unknown base according
3 to said probe associated with said higher probe intensity if
4 said ratio is greater than a predetermined ratio value.

1 5. The method of claim 4, wherein said
2 predetermined ratio value is approximately 1.2.

1 6. In a computer system, a method of identifying
2 an unknown base in a sample nucleic acid sequence, said method
3 comprising the steps of:

4 inputting a first set of probe intensities, each of
5 said probe intensities in said first set being associated with
6 a nucleic acid probe and substantially proportional to said
7 associated nucleic acid probe hybridizing with a reference
8 nucleic acid sequence;

9 inputting a second set of probe intensities, each of
10 said probe intensities in said second set being associated
11 with a nucleic acid probe and substantially proportional to
12 said associated nucleic acid probe hybridizing with said
13 sample sequence;

14 said computer system comparing at least one of said
15 probe intensities in said first set and at least one of said
16 probe intensities in said second set; and

17 calling said unknown base according to results of
18 said comparing step.

1 7. The method of claim 6, wherein said comparing
2 step includes the steps of:

3 calculating first ratios of a wild-type probe
4 intensity to each probe intensity of a probe hybridizing with
5 said reference sequence, wherein said wild-type probe
6 intensity is associated with a wild-type probe; and

7 calculating second ratios of the highest probe
8 intensity of a probe hybridizing with said sample sequence to
9 each probe intensity of a probe hybridizing with said sample
10 sequence.

1 8. The method of claim 7, wherein said comparing
2 step further includes the step of calculating third ratios of
3 said first ratios to said second ratios.

1 9. The method of claim 8, wherein said calling
2 step includes the step of calling said unknown base according
3 to said probe associated with a highest third ratio.

1 10. The method of claim 6, wherein said comparing
2 step includes the step of calculating a ratio of a highest
3 probe intensity in said first set to a highest intensity in
4 said second set.

1 11. The method of claim 10, wherein said comparing
2 step further includes the step of comparing said ratio of
3 neighboring nucleic acid probes.

1 12. In a computer system, a method of identifying
2 an unknown base in a sample nucleic acid sequence, said method
3 comprising the steps of:

4 inputting statistics about a plurality of
5 experiments, each of said experiments producing probe
6 intensities each being associated with a nucleic acid probe
7 and substantially proportional to said associated nucleic acid
8 probe hybridizing with a reference nucleic acid sequence;

9 inputting a plurality of probe intensities, each of
10 said plurality of probe intensities being associated with a
11 nucleic acid probe and substantially proportional to said
12 associated nucleic acid probe hybridizing with said sample
13 sequence;

14 said computer system comparing at least one of said
15 plurality of probe intensities with said statistics; and

16 calling said unknown base according to results of
17 said comparing step.

1 13. The method of claim 12, further comprising the
2 step of calculating said statistics.

1 14. The method of claim 12, wherein said statistics
2 include a mean and standard deviation.

1 15. A method of processing first and second nucleic
2 acid sequences, comprising the steps of:

3 providing a plurality of nucleic acid probes;
4 labeling said first nucleic acid sequence with a
5 first marker;

6 labeling said second nucleic acid sequence with a
7 second marker; and

8 hybridizing said first and second labeled nucleic
9 acid sequences at the same time.

1 16. The method of claim 15, wherein said plurality
2 of nucleic acid probes are on a chip.

1 17. The method of claim 15, further comprising the
2 step of fragmenting said first and second nucleic acid
3 sequences at the same time.

1 18. The method of claim 15, further comprising the
2 step of scanning for said first and second markers on said
3 chip, said first and second labeled nucleic acid sequences
4 being on said chip.

1 19. The method of claim 15, wherein said first and
2 second markers are fluorescent markers that emit light at
3 different wavelengths upon excitation.

1 20. In a computer system, a method of identifying
2 mutations in a sample nucleic acid sequence, said method
3 comprising the steps of:

4 inputting a first set of probe intensities, each of
5 said probe intensities in said first set being associated with
6 a nucleic acid probe and substantially proportional to said
7 associated nucleic acid probe hybridizing with a reference
8 nucleic acid sequence;

9 inputting a second set of probe intensities, each of
10 said probe intensities in said second set being associated
11 with a nucleic acid probe and substantially proportional to

12 said associated nucleic acid probe hybridizing with said
13 sample sequence;
14 said computer system comparing probe intensities in
15 said first set and probe intensities in said second set to
16 select hybridization regions where said probe intensities in
17 said first set and said probe intensities in said second set
18 differ; and
19 identifying mutations according to characteristics
20 of said selected regions.

1 21. The method of claim 20, wherein said selected
2 regions are determined by comparing probe intensities of wild-
3 type probes.

1 22. The method of claim 21, wherein said wild-type
2 probes are complementary to a portion of said reference
3 sequence.

1 23. The method of claim 21, wherein said
2 identifying step further includes the steps of:
3 analyzing a size of a selected region;
4 identifying a likely position of a mutation in said
5 selected region according to an interrogation position of said
6 nucleic acid probes; and
7 performing base calling at said likely position.

1 24. In a computer system, a method of analyzing a
2 plurality of sequences of bases, said plurality of sequences
3 including at least one reference sequence and at least one
4 sample sequence, the method comprising the steps of:
5 displaying said at least one reference sequence in a
6 first area on a display device; and
7 displaying said at least one sample sequence in a
8 second area on said display device;
9 whereby a user is capable of visually comparing said
10 plurality of sequences.

1 25. The method of claim 24, wherein said plurality
2 of sequences are monomer strands of DNA or RNA.

1 26. The method of claim 24, wherein said at least
2 one reference sequence includes a chip wild-type that has been
3 tiled on a chip.

1 27. The method of claim 26, wherein said chip wild-
2 type sequence is displayed as a first sequence in said first
3 area.

1 28. The method of claim 26, further comprising the
2 step of displaying a label in said first area to identify said
3 chip wild-type sequence.

1 29. The method of claim 24, wherein said at least
2 one sample sequence has been hybridized on a chip.

1 30. The method of claim 24, further comprising the
2 step of indicating bases that differ among a plurality of user
3 selected sequences.

1 31. The method of claim 24, further comprising the
2 steps of:
3 displaying a name associated with each of said at
4 least one reference sequence in said first area; and
5 displaying a name associated with each of said at
6 least one sample sequence in said second area.

1 32. The method of claim 24, further comprising the
2 step of linking at least one reference sequence in said first
3 area with at least one sample sequence in said second area.

1 33. The method of claim 32, further comprising the
2 step of indicating on said display device which sequences are
3 linked.

1 34. The method of claim 24, further comprising the
2 step of indicating bases of said at least one sample sequence
3 that are not equal to a corresponding base in said at least
4 one reference sequence.

1 35. The method of claim 24, wherein said at least
2 one reference sequence and said at least one sample sequence
3 are aligned on said display device.
hybridization with said probes.